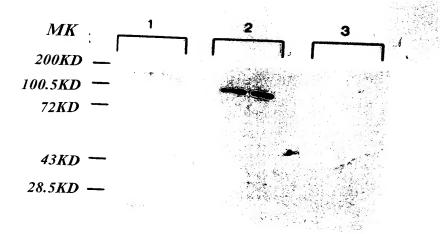
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FIGURE 1

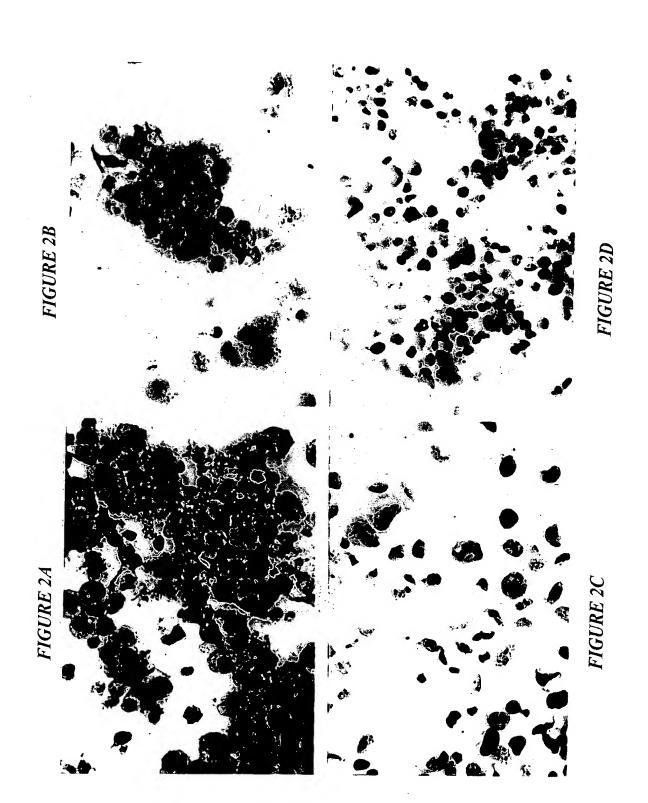


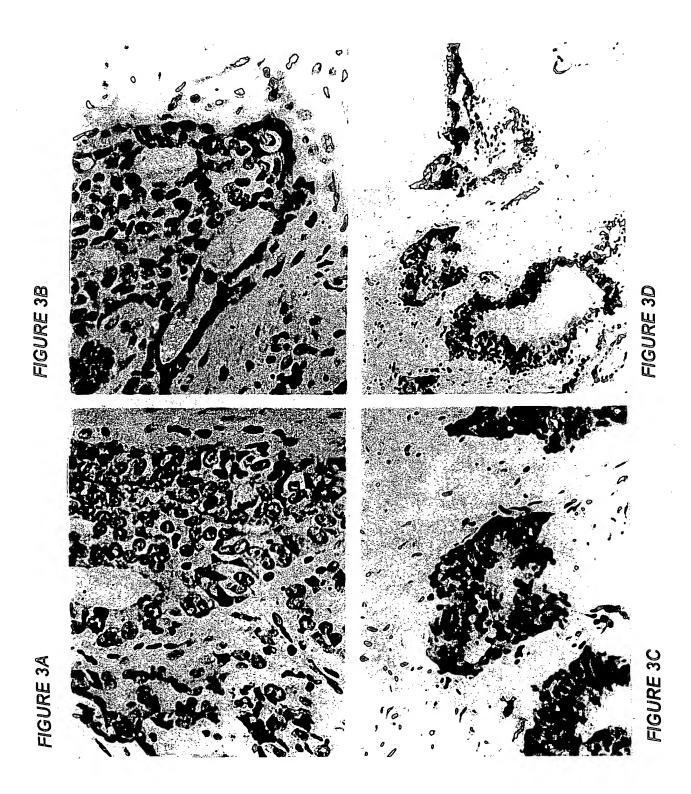
1 - anti- EGFr PoAB RK-2

2 - Cyt-356 MoAB/RAM

3 - RAM

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FIGURE 4

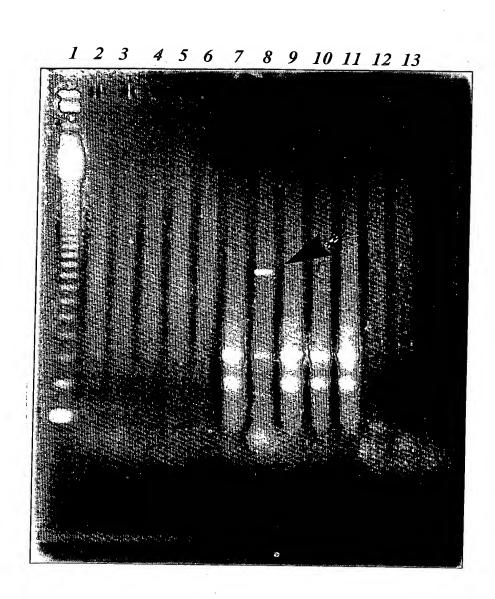
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72.0

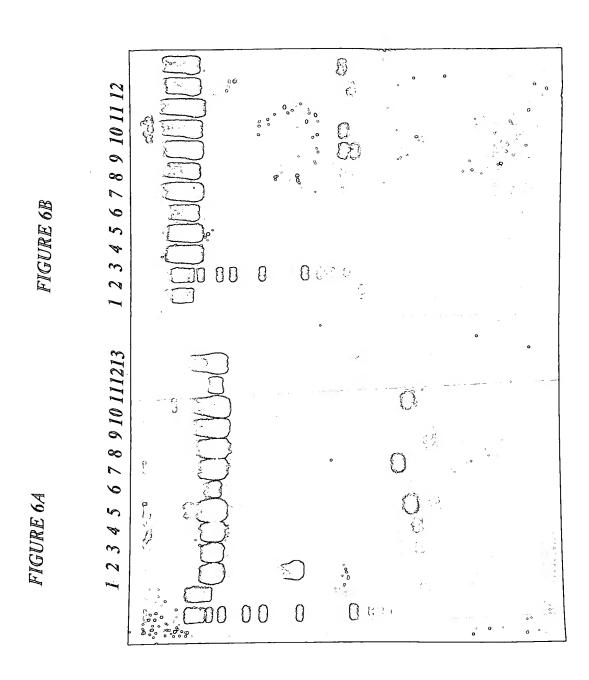
43.0

28.5

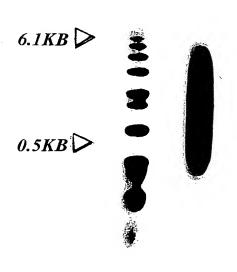
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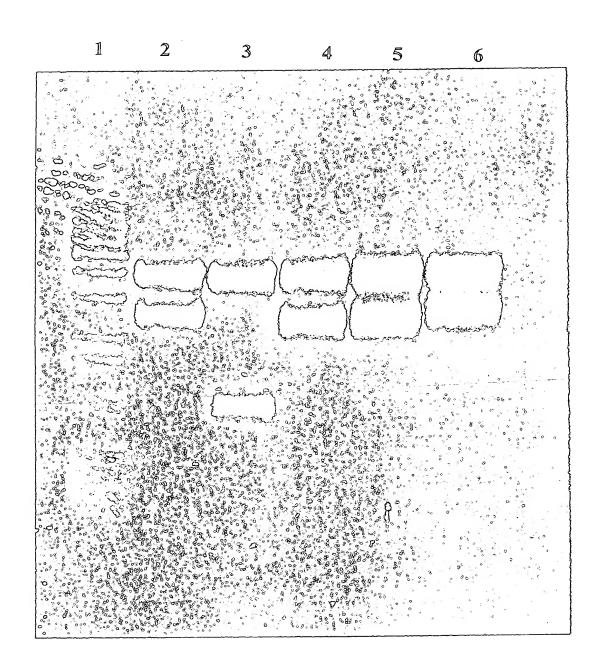
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FIGURE 9

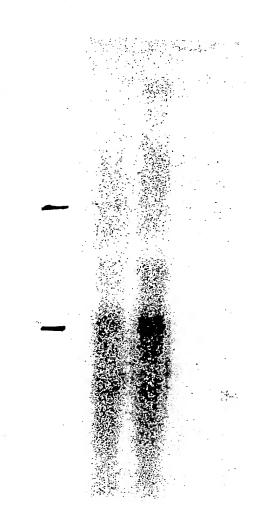
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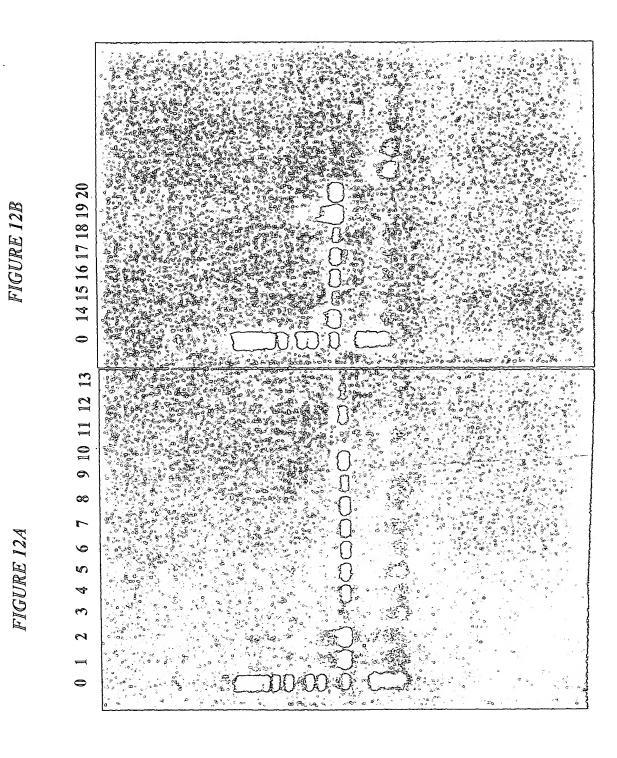


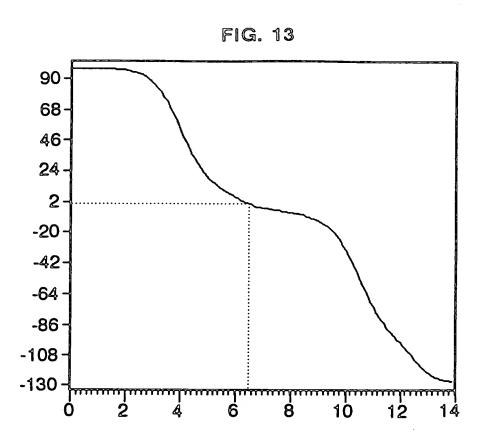
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FIGURE 11

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FIG. 14-1

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FIG. 14-3

semi-graphical representation: Symbols used in the

FIG. 14-4

Semi-graphical output.

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conformation:

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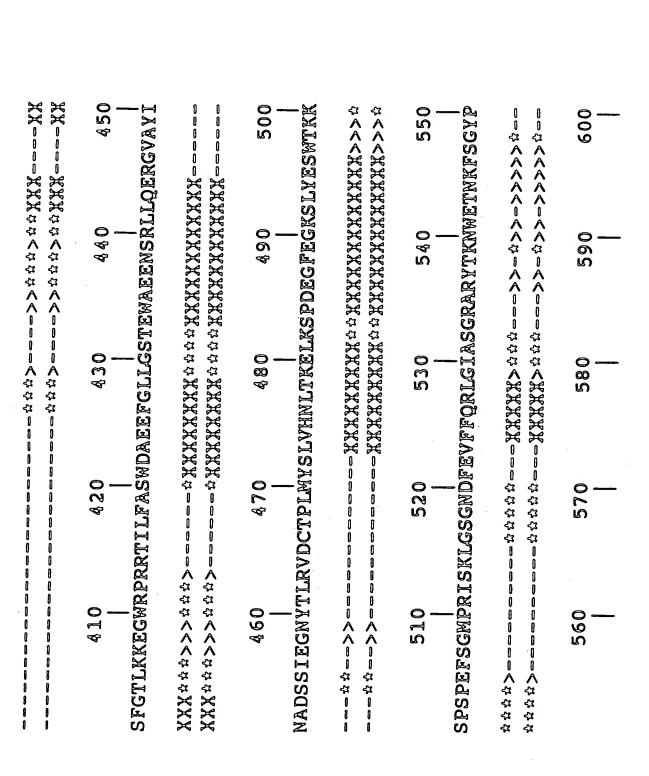
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LYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	ETYELVEKFYDPMFKYHLTVA XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	ILTVAQVRGGM X-X X-X	VFELANSIVLF XXXXX XXXXX	>FDCRDY > XXX > XXX
AVVLRKYADKIYSISMKHPQEMKTYSVSFDSLFSAVKNFTEIASKFSERL XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	ISMKHPQEMKT X**XXXXK- X**XXXXK-	TYSVSFDSLF [XXX		IRFSERL (XXXXXX (XXXXXX
660 670 680 690 700 QDFDKSNPIVLRMMNDQLMCLERAFIDPLGLPDRPFYRHVIYAPSSHNKY	670 - WNDQLMCLEF	680 VAFIDPLGLPD	690 RPFYRHVIYAF	700 SSHNKY
XX>>>\$\phi\$ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	-<\$\$\$\$<<>XXXXXXXXXXX>>	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
710 720 730 740 750 AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA	720 DIESKVDPSI	730 Kawgevkrqiy	740 Vaaftvqaaae	750 TLSEVA
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FIG. 15A

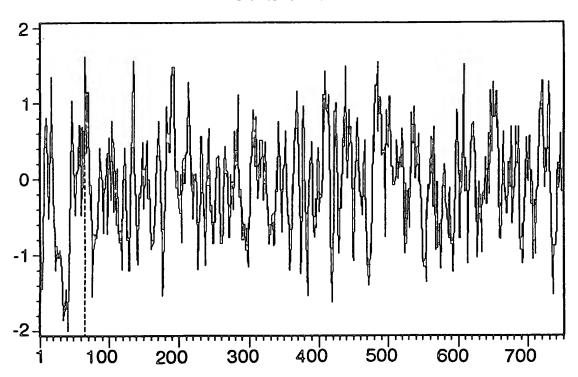


FIG. 158

Done on saquence PMSANTIGEN. Total number of residues is: 750. Analysis done on the complete sequence

authors The averaging group length is: 6 amino acids. The method used is that of Hopp and Woods. by the the value recommended . ໝ -> This

3 KB: highest points of hydrophilicity three The

Asp-Glu-Lau-Lys-Ala-Glu Asn-Glu-Asp-Gly-Asn-Glu <u>ම</u> ග 137 r O 132 From From 1.62 1.57

Lys-Ser-Pro-Asp-Glu-Gly 60 800 From

Ah stands for: Average hydrophilicity.

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1220 CAGCTGGAGAGG : :::: ::: GTTGGAAAGG	1280 TCTACACAAA : : : : : : : : : : GCCAGA-TAA	1340 GTGATAGGTAC : ::: : ATCTTCGGTGC	1400 1410 CGGACTCATGGGTGTTT : ::::::::::::::::::::::::::::
1210 CACCAGATAGO : :: :: GCTCTGA-AG-	1260 1270 CTTTACTGGAAACTTT CAAAGCAGGAGA	1330 AATTTACAATG ::: GATTCTGAACA	1390 3GGAGGTCACC 3333 3340
1200 AGCAC :: CACAT	1260 CTTTAC ; CAAAGC	1320 GACAAG ; ; CAGGAA	1380 CATTCTG : : TGTGATT
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1440 1450 1460 1470 1480 1490 AGCTGTTGTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAGGAAGGGTGGAG :::::::::::::::::::::	1500 1510 1520 1530 1540 1550 ACCTAGAAGAACTTTGTTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTTGTTTC ::::::::::::::::::::::::	1560 1570 1580 1590 1600 1610 TACTGAGTGGGCAGAGTTCAAGACTCCTTCAAGAGCGTGGCCTTATATTAA :::::::::::::::::::::::::::	1620 1640 1650 1670 1670 1670 1620 1670 TGC-TGACTCATCTATAGAAGGAAACTA-CACTCTGAGATTGATTGTACACCGCTGATG :::::::::::::::::::::::::::::::::
1480 .149 CACTGAAAAGGAAGGGT ; ;;;;;;;;; TAGTGAAAACGAGGGCT 1430 .1440	1540 AAGAATTTGGI ::: : :: GAGACTACGG? 1490	1600 AGCGTGGCGTGG ; ; CCAAAGCTTTCA 1550	0 1660 AGTTGATTGTA :: : : GATTTCTGCCA 1610
1470 GAGCTTTGGAAC :: :: : GATCTCAGACAT 1420	1530 CTGGGATGCAG	1590 ACTCCTTCAAG : :: :: : CATGCTGCATG	1640 GGAAACTA-CACTCTGAGAG :: : : : : : : : : : : : : : : : : : :
1460 TTGTGAGC	1520 TGTTTGCAAGG XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	1570 1580 SAGGAGAATTCAAG SSGGGTACTCTGC 1530	GAAGGAAACTA SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
1450 IGTTCATGAAA : : : : ATTGTTGGAAC 1400	1510 AAGAACAATTT ::: CGAAGCATCA:	1570 TGGGCAGAGG ::: : :::	20 1630 ACTCATCTATAG : :: : SATGCTCCAGTC
pmsgen CHKTFE	pmsgen	pmsgen CHKTFE	pmsgen CHKTFE

1730 LAGGC :: GAGC	790 GCCC	TGGA
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CCCTGA TCCAGO	0 CCCAGA	lagcagitg 1720
1710 CAAAAGCC :::: : CAAGAATC	1770 TCCTTCCC	Taaaag 1
1700 AAGAGCT : : : AGGGGGT 50	1760 Aaaaaag :	ACTGGGT 1710
raacaaz : : :: Tratgaz	1750 AGTTGGACTAAAA : :::: : : :	GCCCAG, 0
1690 ACAACC ; ; GAGTA1	1750 AAGTTG	GACTTG 170
BO FGGTACA FGCTGG	O TTATGA	ataaca 690
1680 1690 1700 1710 1720 1730 1730 1730 1730 1730 1730 1730 173	pmsgen AAATCTCTTTATGAAAGTTGGACTAAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCC	CICTATAACAGACTTGGCCCAGACTGGGTAAAAGCAGTTGTTCCTCTTGGCCTGGA 1710 1720 1730
	n AA	
pmsg(CHKTF	pmsgen	

311		
164	rggct: : : :: ragat:	o ATG ATGTA(
164	1250 TGTTGGACC' ; ; ; GTTGGAATA'	1310 CATC-CACTCT-ACCAATG : :::: : ::::: AAGCTCACTGTGAACAATG
3' end.	1250 AAAGTGCCCTACAATGTTGGACCTGGCT' ::: :: :: :: : : : : : : : : : : : : :	1300 GCACATC-CA(: : : : : : : : : : : : : : : : : : :
r mRNA, p	1230 TCTCAAAG :::: AAGGAAAC	80 CAAAAGTCAAGATGC ::::::::::::::::::::::::::::::::::::
TTRFR Rat transferrin receptor mRNA, 3' end. 55.5% identity in 560 nt overlap	1220 rggaggaag caaaaacatgg 630	1260 1270 1280 1290 1300 1310 pmsgen -TACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATC-CACTCT-ACCAATG ; ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;
Rat transfer entity in 56	1210 pmsgen CCACCAGATAGCAGCT RATTRF TGCAGAAAAGCTATTC	1270 CTGGAAACTTT :: :: :: ATGTAAGCTGG
RATTRFR 55.5% id	pmsgen CCA RATTRF TGC 610	1260 pmsgen -TA ° RATTRF CTC 670

1370 CAGACAG :::::::	1430 STCAGAG SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	1480 -AAAAGGAA ::: :: rcaaaagat 00	SGTCTT
1360 137 137 137 1380 130	1420 ATTGACCC :: TGCGAAG1 840	1480 TGAAAAA SSS SSSSSSSSSSSSSSSSSSSSSSSSSSS	1530 1540 TGCAGAAGAATTTGG :::::::::::::::::::::::::::
1320 1330 1340 1350 1360 1370 pmsgenAAGTGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAG iii iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	1380 1390 1400 1410 1420 1430 1430 1430 1430 1430 1430 1430 143	1440 1450 1460 1470 1480 pmsgen T-GGAGCTGTGTTCATGAAATTGTGAGGAGCTTTGGAACA-CTGAAAAAGGAA iiiiiiiiiiiiiiiiiiiiiiiiiii	
1340 TAGGTACTCTCAGAGGAG : :: : : ::: TTGGCGTTATTAAAGGCT 760 770	1400 141 GACTCATGGGTGTT :::::::: GACGCTTGGGGCCC 820 8	O 1 GGAGCTTT :: :: CAAGTATT 880	1510 ATTTTGTTTGCAAGCTGGGA ::::::::::::::::::::::::::::::::::
1340 STGATAGGT S S S ATCTTTGGC	1400 CGGACTCA' : ::: : AGAGACGCT' 820	1460 AATTGTGAG	1510 ATTTTGTTT ::: :::: ATTATCTTTC
1330 TTACAATGTC ; ; ; ACTTAACATC	1390 GGAGGTCACC :::: :: GGAGCCCAGA	1450 TTCATGAAATT : :::::: CTGTTGAAACT 870	0 AAGAACAAT ;;;;;; CAGGAGTAT
1320 Gacaagaat :::::::::	1380 CATTCTGGG : : : : : : : : : : : : : : : : : :	1440 AGCTGTTG :: :: AGGTCTT-	1500 AGACCTAGA X:::::::
nAAGTG ::: F GAAAGAA	1380 pmsgen ATATGTCATTCTG	144 T-GGAGCAGC : ::: ::: TGGGAACAGG	1490 150 GGGTGGAGACCTA(:: X:::: ; GGATTTAGACCCA(910 920
pmsgen RATTRF	pmsgen RATTRF 75	pmsgen RATTRF	pmsgen RATTRF

1550 1560 1570 1580 1590 1600 CTTGGTTCTACTGAGTGGGAGAGAGAGACTCCTTCAAGAGCGTGGCGTG :::::::::::::::::::::::::::::	1610 1620 1640 1650 1660 pmsgen GCTTATATGACTCATCTATAGAAGGAAACTA-CACTCTGAGAGTTGATTGTAC :::::::::::::::::::::::::::::::::::	1670 1680 1690 1700 1710 1720 ACCGCTGATGTACACCAACCTAACAAAGGCTGAAAAGC-CCTGATGAAG :: :: : : : : : : : : : : : : : : : :
560 1570 GAGTGGCCAGAGGAA- ::::::: X GAGTGGCTGGAGGGGTAC	1630 TCTATAGAA ; AGTCGTCCT	1690 ACACAACCT. : : : GGGGAAGAT.
1560 TACTGAGTGGGC :::::::::: GACTGAGTGGCT	1620 ATGCTGACTCAT :::::::	1680 TACAGCTTGGT :: : : : : : : : : : : : : : : : : : :
	1610 GCTTATATTAATG :::::::::: ACTTACATTAAT-	1670 ACCGCTGATGT :: :: : : : CCCCTATTAT
pmsgen Rattr	pmsgen Rattr	pmsgen ; RATTRF (

	1730	1740		1750	1760	1770
pmsgen	GCTTTGAAGG	CAAATCTCTI	TAT-GAA	AGTTGGAC	TAAAAAAG	pmsgen GCTTTGAAGGCAAATCTCTTTAT-GAAAGTTGGACTAAAAAAAGTCCTTCCCAG
	000000000000000000000000000000000000000		000000000000000000000000000000000000000	00		0.0
RATTRF		AAAATATCTA	TATCGAAACA	GTAATTGGAT	TAGCAAAAT	TTGATGGAAATATCTATATCGAAACAGTAATTGGATTAGCAAAATTGAGGAACTTT
	1140	1150	1160	1170	1180	1190
	1780	1790	1800	1810	1820	1830
pmsgen	AGTTCAGTGG	CATGCCCAGG	ATAAGCAAAT	TGGGATCTGG	AAATGATTT	pmsgen AGTTCAGTGCCATGCCAGGATAAGCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCT
RATTRF	CCTTGGACAA	IGCTGCATTC	CCTTTTCTTG	CATATTCAGG	BATCCCAGC	RATTRF CCTTGGACAATGCTGCATTCCCTTTTCTTGCATATTCAGGAATCCCAGCAGTTTCTTTC
	7200	1210	1210 1220 1230 1240 1250	1230	しゃくに	כער

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145	A T	1330 TACA CTTA	1390 667 670	14 ICA
4			& D	£ 5
ደ የ	o TGC 90	# # O		o TGTT TCTC 1370
~	1270 AACTT GGATG 1190	0 !AAGA! :: : !AAAA! 1250	O TCTG ; AGTT 1310	40 CTC
ත ව	0 TAC-TGGAAA ::: :: : TACATGTAGG	1320 AAGTGACAAGAATT ::: :: :::: AAGAGATAAAAATT 0	1380 139 TATGTCATTCTGGGAGGT :::::: ; ; ; ; TATGTTGTAGTTGGGGCC 1310	1440 CAGCTGTTC :::::: CAGCTCTCC
complete cd	Ď Ď		GTC	AGC CAC
ے 0		-A.A.	FAT FAT TAT	T-GG. TAGG. 1360
Q E	1260 CTTTAC:::::::CTCTAC	A : TGAA 1240	OGATA ::: ACTA	
ບິ	126 3CTT 3CTC	ာ ၁၅	1370 ACAG * ATCA	1430 AGAG : :
A.	CTGG CAGA	H	\$ \$ \$	
Human transferrin receptor mRNA, entity in 464 nt overlap	*	0 CACTCT-ACCAATG :::::::::::::::::::::::::::::::::::	1360 GTGGAACCAGACA :: :::::: GTAGAACCAGATC	1430 SACCCTCAGAGT-GGA ; ; ; ; ; ; ; ; AAATC-CGGTGTAGGC 1350
ង	1250 TTGGAC GGAAAA	131 ACCA : :: AGCA 1230	0 GAAC GAAC 1290	O GACC : AAAT 1350
ည် တိ	1115 1117 1118		1360 GTGG GTAG	1420 ATTG GCAA
C C C	A C	CI CI	CAC FFG	0
rrin recept nt overlap	2 2 3 3 6 8	0 2 : 2 0	S S S S S S S S S S S S S S S S S S S	O TGGTGGT :::::::: TGGAGCT
it i	1240 CCCTAC CCCTCT	1300 1700 1750 1750 1750	350 AGAGGA : ::: AAAGGC	0 TGGT TGGA 1340
H H H H H H	င္က ည လည္သ	CA.	1350 CAGAC TAAAC	1410 GTTT
88 67 64	GT TGI			
	LAA 1900	A TG		9 9 9 9
Human transfe identity in 464	30 TCAA GAGA 1150	1290 Caaga aagaa 1210	o Gtac' : Gagt' 1270	OCATGGG SESTEGG CATGGG
E i	1230 FTCTC	C C H	1340 TAGG	1400 ACTC ATGC
HUN Pun	0	aaagt aaagc	IAT.	14 GGAC
ି 'ପି •=	S A O			Ů Š
85 85 85 85 85 85	in AG('R TA: 1140	1280 en AA : : FR AG 1200	n TG R CA	ы СС(1320
mtfrr 54 . 3%	9 E			0 E
HUMTFRR 54.3%	1230 1240 1250 1260 1270 Pmsgen AGGAAGTCTCAAAGTGCTTAGACCTGGCTTTAC-TGGAAACTTTTCTACAC i i i i i i i i i i i i i i i i i i i	1280 1290 1300 1310 1320 1330 1330 1330 1330 133	1340 1350 1350 1390 1390 1390 1390 1390 1390 pmsgen TGTGATACTCTCGGAGGTCA 1390 1390 1390 1390 1390 1390 1390 1300 1260 1250 1250 1250 1250 1250 1310	1400 1410 1430 1440 1450 pmsgen CCGGGACTCATTGGTGTATTGACCCTCAGAGT-GGAGCAGCTGTTGTTCATG ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
, =	124 144	보 프	으 표	Q X

1460 1470 1480 1490 1500 pmsgen AAATTGTGAGGACTTTGGAACACTGAAAAAGGAAGGTGGAGACCTAGAACAA iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	1510 1520 1530 1540 1550 1560 TTTTGTTTGCAAGAATTTGGTCTTCTTACTGAGGGCAG :: ::::::::::::::::::::::::::::::::::	1570 1580 1590 1600 1610 1620 A-GGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTTATTAATGCTGACTCATCT : ::::::::::::::::::::::::::::::::::	1630 1640 1650 1660 1670 1680 ATAGAAGGAAACTACACTCTGAGAGTTGATGATGTACA-GCTTGGT-AC
480 1490 AAAAGGAAGGGTGGAG ::::X::: TAAAAGATGGGTTTCA	1550 CTTCTTGGTTCT :::::: :TCGGTTGGTGCC	1610 GGCTTATATTAAT :::::::X CACTTATATTAAT	1670 ACCGCTGATGTA ::::::::::::::::::::::::::::::::
1480 ACACTGAAAAAG 	1540 AAGAATTTGGT :::::::: GAGACTTTGGA	1600 GAGCGTGGCGT ; ; TTAAAGGCTTT 1530	1660 GTTGATTGTAC ::: ; ; ; GTTTCTGCCAG
1470 GAGCTTTGGAA : : : : GTTCTCAGATA	1530 CTGGATGCAGAAGA ::: ::: ::: TTGGAGTGCTGGAGA	1590 CACTCCTTCAA(CACTCCATT CACTCCATT	1650 ACACTCTGAGA(:: : : SCAACTTCAAG(
1460 pmsgen AAATTGTGAG	1520 TGTTTGCAAG : ::::: :: TCTTTGCCAG	70 158 CGAGAATTCAAC	0 1640 GAAGGAAACTA :: : : CTTGGTACCAG
pmsgen AAA :: HUMTFR AAC 1380	1510 pmsgen TTT :: HUMTFR TTA	1570 pmsgen A-GG : :: HUMTFR AGGG	1630 pmsgen ATAG : HUMTFR GTTC' 1560

FIG. 16-10

	∂ n o d d			O 1/2 / 1/2	೨೯/ ₹	O 8 / ⊣
pmsgen	ACAACCTAACAA	racaaaagagc!	TGAAAAGCCCT	ICATCAAGGC	ITTGAAGGCA	AAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATG
	00	00				
HUMTER	AAAACAATGCAAAA	IGCAAAATGTG	AAGCATCCGG	TTACTGGGCA1	ATTTCTATA	ATGTGAAGCATCCGGTTACTGGGCAATTTCTATATCAGGACAGCAAC
	1620	1630	1640	1650	1660	1670

FIG. 16-11

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FIGURE 17A

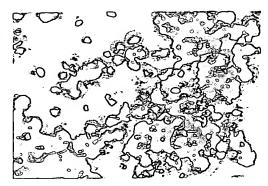


FIGURE 178

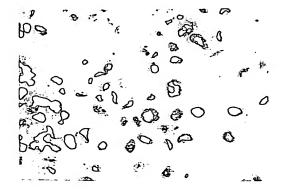
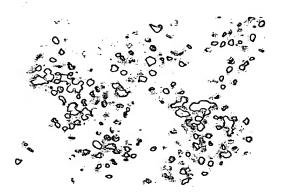


FIGURE 17C

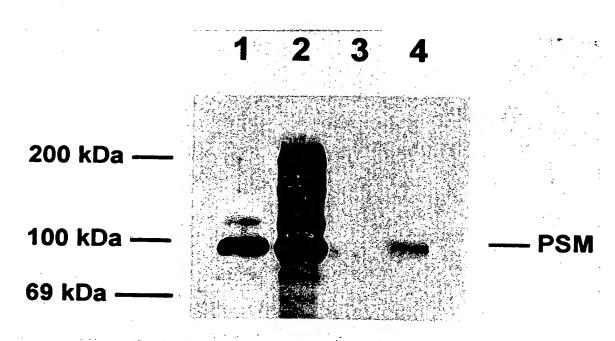


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FIGURE 18

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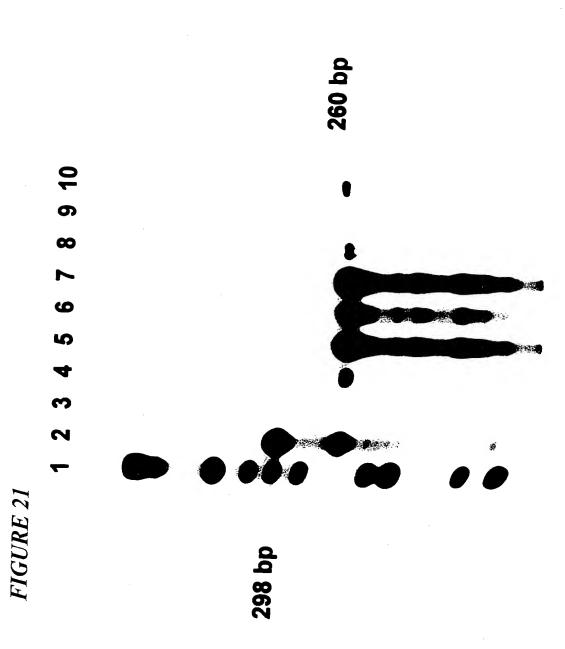


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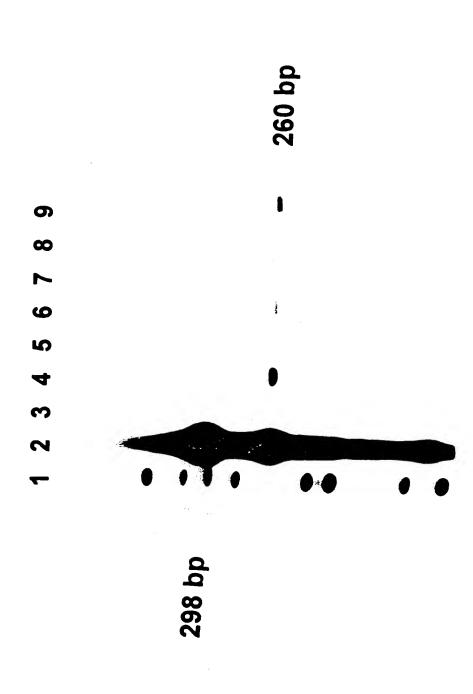
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CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	_	_
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	_	-
R1564 (RAT MAMMARY)	NO	YES	_	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

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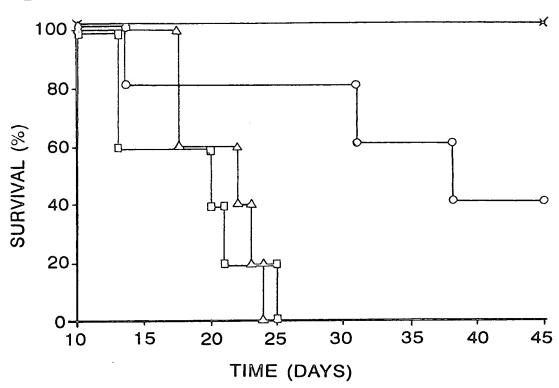
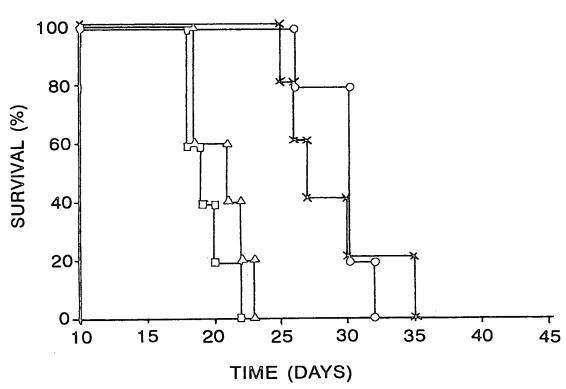


FIGURE 24B



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FIGURE 25A

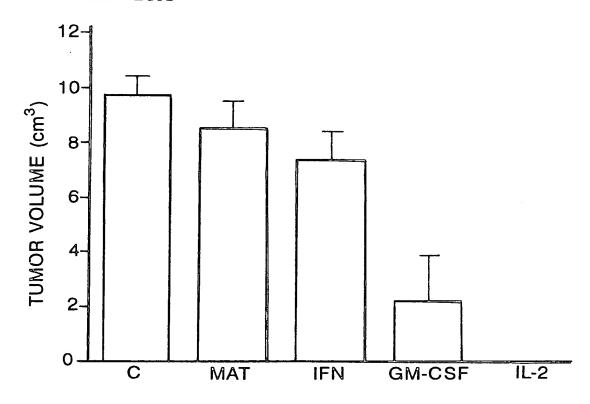
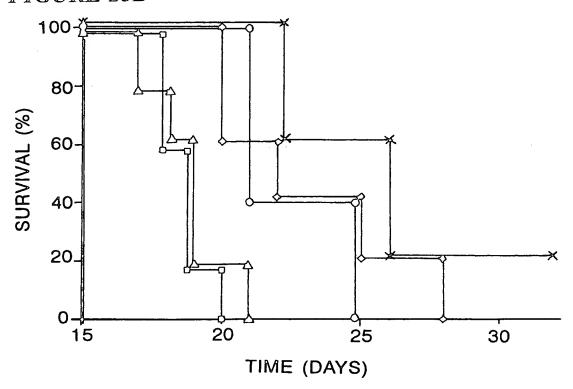
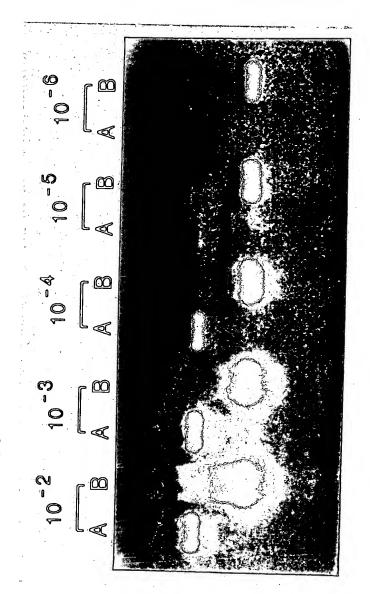


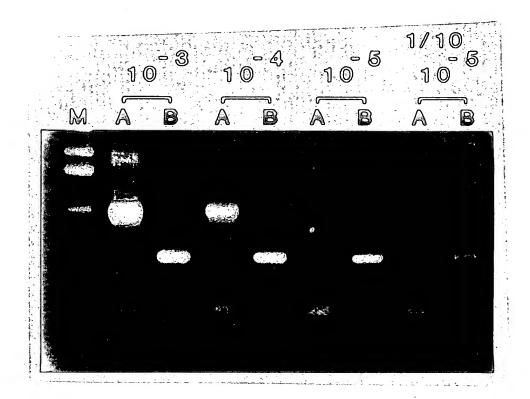
FIGURE 25B



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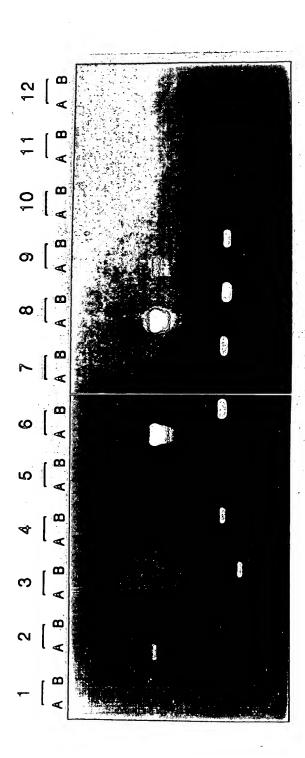


FIGURE 28

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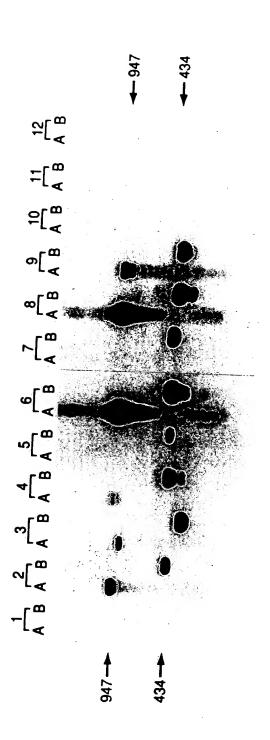


FIGURE 29

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Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	_	+
2	T2NoMo	RRP 7/93	6.1	_	_	+
3	T2CNoMo	PLND 5/93	4.5	0.1	_	+
4	T2BNoMo	RRP 3/92	NMA	0.4	_	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	_	+
6	Recur T3	I-125 1986	54.7	1.4	_	+
7	T3ANoMo	RRP 10/92	NMA	0.3	_	+
8	ТЗПхМо	XRT 1987	7.5	0.1	_	_
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	_
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	_	+
13	ТЗМоМо	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	_	_
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	_
15	D1	Proscar + Flutamide	20.8	0.5	_	_
16	T2CNoMo	RRP 4/92	0.1	0.3	-	-

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